

ccggagagcc ccggagtgag cggagtagcg agtcggcaac ccggaggggt agaaatattt 60

ctgtc atg gct cat tca aag act agg acc aat gat gga aaa att aca tat 110
Met Ala His Ser Lys Thr Arg Thr Asn Asp Gly Lys Ile Thr Tyr
1 5 10 15

ccg cct ggg gtc aag gaa ata tca gat aaa ata tct aaa gag gag atg 158
Pro Pro Gly Val Lys Glu Ile Ser Asp Lys Ile Ser Lys Glu Glu Met
20 25 30

gtg aga cga tta aag atg gtt gtg aaa act ttt atg gat atg gac cag 206
Val Arg Arg Leu Lys Met Val Val Lys Thr Phe Met Asp Met Asp Gln
35 40 45

gac tct gaa gaa gaa aag gag ctt tat tta aac cta gct tta cat ctt 254
Asp Ser Glu Glu Glu Lys Glu Leu Tyr Leu Asn Leu Ala Leu His Leu
50 55 60

gct tca gat ttt ttt ctc aag cat cct ggt aaa gat gtt cgc tta ctg 302
Ala Ser Asp Phe Phe Leu Lys His Pro Gly Lys Asp Val Arg Leu Leu
65 70 75

gta gcc tgc tgc ctt gct gat att ttc agg att tat gct cct gaa gct 350
Val Ala Cys Cys Leu Ala Asp Ile Phe Arg Ile Tyr Ala Pro Glu Ala
80 85 90 95

cct tac aca tcc cct gat aaa cta aag gat ata ttt atg ttt ata aca 398
Pro Tyr Thr Ser Pro Asp Lys Leu Lys Asp Ile Phe Met Phe Ile Thr
100 105 110

aga cag ttg aag ggg cta gag gat aca aag agc cca caa ttc aat agg 446
Arg Gln Leu Lys Gly Leu Glu Asp Thr Lys Ser Pro Gln Phe Asn Arg
115 120 125

tat ttt tat tta ctt gag aac att gct tgg gtc aag tca tat aac ata 494
Tyr Phe Tyr Leu Leu Glu Asn Ile Ala Trp Val Lys Ser Tyr Asn Ile
130 135 140

tgc ttt gag tta gaa gat agc aat gaa att ttc acc cag cta tac aga 542
Cys Phe Glu Leu Glu Asp Ser Asn Glu Ile Phe Thr Gln Leu Tyr Arg
145 150 155

FIG. 1-1

acc tta ttt tca gtt ata aac aat ggc cac aat cag aaa gtc cat atg	590
Thr Leu Phe Ser Val Ile Asn Asn Gly His Asn Gln Lys Val His Met	
160 165 170 175	
cac atg gta gac ctt atg agc tct att att tgt gaa ggt gat aca gtg	638
His Met Val Asp Leu Met Ser Ser Ile Ile Cys Glu Gly Asp Thr Val	
180 185 190	
tct cag gag ctt ttg gat acg gtt tta gta aat ctg gta cct gct cat	686
Ser Gln Glu Leu Leu Asp Thr Val Leu Val Asn Leu Val Pro Ala His	
195 200 205	
aag aat tta aac aag caa gca tat gat ttg gca aag gct tta ctg aag	734
Lys Asn Leu Asn Lys Gln Ala Tyr Asp Leu Ala Lys Ala Leu Leu Lys	
210 215 220	
agg aca gct caa gct att gag cca tat att acc act ttt ttt aat cag	782
Arg Thr Ala Gln Ala Ile Glu Pro Tyr Ile Thr Thr Phe Phe Asn Gln	
225 230 235	
gtt ctg atg ctt ggg aaa aca tct atc agc gat ttg tca gag cat gtc	830
Val Leu Met Leu Gly Lys Thr Ser Ile Ser Asp Leu Ser Glu His Val	
240 245 250 255	
ttt gac tta att ttg gag ctc tac aat att gat agt cat ttg ctg ctc	878
Phe Asp Leu Ile Leu Glu Leu Tyr Asn Ile Asp Ser His Leu Leu Leu	
260 265 270	
tct gtt tta ccc cag ctt gaa ttt aaa tta aag agc aat gat aat gag	926
Ser Val Leu Pro Gln Leu Glu Phe Lys Leu Lys Ser Asn Asp Asn Glu	
275 280 285	
gag cgc cta caa gtt gtt aaa cta ctg gca aaa atg ttt ggg gca aag	974
Glu Arg Leu Gln Val Val Lys Leu Leu Ala Lys Met Phe Gly Ala Lys	
290 295 300	
gat tca gaa ttg gct tct caa aac aag cca ctt tgg cag tgc tac ttg	1022
Asp Ser Glu Leu Ala Ser Gln Asn Lys Pro Leu Trp Gln Cys Tyr Leu	
305 310 315	
ggc agg ttt aat gat atc cat gta cca atc cgc ctg gaa tgt gtg aaa	1070
Gly Arg Phe Asn Asp Ile His Val Pro Ile Arg Leu Glu Cys Val Lys	
320 325 330 335	

FIG. 1-2

ttt gct agc cat tgt ctc atg aac cat cct gat tta gca aaa gac tta	1118
Phe Ala Ser His Cys Leu Met Asn His Pro Asp Leu Ala Lys Asp Leu	
340 345 350	
aca gag tat ctt aaa gtg agg tca cat gac cct gag gaa gct att aga	1166
Thr Glu Tyr Leu Lys Val Arg Ser His Asp Pro Glu Glu Ala Ile Arg	
355 360 365	
cat gat gtt att gtg tca ata gtt aca gct gct aaa aag gat att ctt	1214
His Asp Val Ile Val Ser Ile Val Thr Ala Ala Lys Lys Asp Ile Leu	
370 375 380	
ctg gtc aat gat cac tta ctt aat ttt gtg aga gag aga aca tta gac	1262
Leu Val Asn Asp His Leu Leu Asn Phe Val Arg Glu Arg Thr Leu Asp	
385 390 395	
aaa cga tgg aga gta cgc aaa gaa gcc atg atg gga ctt gcc caa att	1310
Lys Arg Trp Arg Val Arg Lys Glu Ala Met Met Gly Leu Ala Gln Ile	
400 405 410 415	
tat aag aaa tat gct tta cag tca gca gct gga aaa gat gct gca aaa	1358
Tyr Lys Lys Tyr Ala Leu Gln Ser Ala Ala Gly Lys Asp Ala Ala Lys	
420 425 430	
cag ata gca tgg atc aaa gac aaa ttg cta cat ata tat tat caa aat	1406
Gln Ile Ala Trp Ile Lys Asp Lys Leu Leu His Ile Tyr Tyr Gln Asn	
435 440 445	
agt att gat gat cga cta ctt gtt gaa cgg atc ttt gct caa tac atg	1454
Ser Ile Asp Asp Arg Leu Leu Val Glu Arg Ile Phe Ala Gln Tyr Met	
450 455 460	
gtt cct cac aat tta gaa act aca gaa cgg atg aaa tgc tta tat tac	1502
Val Pro His Asn Leu Glu Thr Thr Glu Arg Met Lys Cys Leu Tyr Tyr	
465 470 475	
ttg tat gcc aca ctg gat tta aat gct gtg aaa gca ttg aat gaa atg	1550
Leu Tyr Ala Thr Leu Asp Leu Asn Ala Val Lys Ala Leu Asn Glu Met	
480 485 490 495	
tgg aaa tgt caa aat ctg ctc cga cat caa gta aag gat ttg ctt gac	1598
Trp Lys Cys Gln Asn Leu Leu Arg His Gln Val Lys Asp Leu Leu Asp	
500 505 510	

FIG. 1-3

ttg att aag caa ccc aaa aca gat gcc agt gtc aag gcc ata ttt tca	1646
Leu Ile Lys Gln Pro Lys Thr Asp Ala Ser Val Lys Ala Ile Phe Ser	
515 520 525	
aaa gtg atg gtt att aca aga aat tta cct gat cct ggt aag gct cag	1694
Lys Val Met Val Ile Thr Arg Asn Leu Pro Asp Pro Gly Lys Ala Gln	
530 535 540	
gat ttc atg aag aaa ttc aca cag gtg tta gaa gat gat gag aaa ata	1742
Asp Phe Met Lys Lys Phe Thr Gln Val Leu Glu Asp Asp Glu Lys Ile	
545 550 555	
aga aag cag tta gaa gta ctt gtt agt cca aca tgc tcc tgc aag cag	1790
Arg Lys Gln Leu Glu Val Leu Val Ser Pro Thr Cys Ser Cys Lys Gln	
560 565 570 575	
gct gaa ggt tgt gtg cgt gaa ata act aag aag ttg ggc aac ccc aaa	1838
Ala Glu Gly Cys Val Arg Glu Ile Thr Lys Lys Leu Gly Asn Pro Lys	
580 585 590	
cag cct aca aat cct ttc ctg gaa atg atc aag ttt ctc ttg gag agg	1886
Gln Pro Thr Asn Pro Phe Leu Glu Met Ile Lys Phe Leu Leu Glu Arg	
595 600 605	
ata gca cct gtg cac ata gat acc gaa tct atc agt gct ctt att aaa	1934
Ile Ala Pro Val His Ile Asp Thr Glu Ser Ile Ser Ala Leu Ile Lys	
610 615 620	
caa gtg aac aaa tca ata gat gga aca gca gat gat gaa gat gag ggt	1982
Gln Val Asn Lys Ser Thr Asp Gly Thr Ala Asp Asp Glu Asp Glu Gly	
625 630 635	
gtt cca act gat caa gcc atc aga gca ggt ctt gaa ctg ctt aag gta	2030
Val Pro Thr Asp Gln Ala Ile Arg Ala Gly Leu Glu Leu Leu Lys Val	
640 645 650 655	
ctc tca ttt aca cat ccc atc tca ttt cat tct gct gaa aca ttt gaa	2078
Leu Ser Phe Thr His Pro Ile Ser Phe His Ser Ala Glu Thr Phe Glu	
660 665 670	
tca tta ctg gct tgt ctg aaa atg gat gat gaa aaa gta gca gaa gct	2126
Ser Leu Leu Ala Cys Leu Lys Met Asp Asp Glu Lys Val Ala Glu Ala	
675 680 685	

FIG. 1-4

gca cta caa att ttc aaa aac aca gga agc aaa att gaa gag gat ttt	2174
Ala Leu Gln Ile Phe Lys Asn Thr Gly Ser Lys Ile Glu Glu Asp Phe	
690 695 700	
cca cac atc aga tca gcc ttg ctt cct gtt tta cat cac aaa tct aaa	2222
Pro His Ile Arg Ser Ala Leu Leu Pro Val Leu His His Lys Ser Lys	
705 710 715	
aaa gga ccc ccc cgt caa gcc aaa tat gcc att cat tgt atc cat gcg	2270
Lys Gly Pro Pro Arg Gln Ala Lys Tyr Ala Ile His Cys Ile His Ala	
720 725 730 735	
ata ttt tct agt aaa gag acc cag ttt gca cag ata ttt gag cct ctg	2318
Ile Phe Ser Ser Lys Glu Thr Gln Phe Ala Gln Ile Phe Glu Pro Leu	
740 745 750	
cat aag agc cta gat cca agc aac ctg gaa cat ctc ata aca cca ttg	2366
His Lys Ser Leu Asp Pro Ser Asn Leu Glu His Leu Ile Thr Pro Leu	
755 760 765	
gtt act att ggt cat att gct ctc ctt gca cct gat caa ttt gct gct	2414
Val Thr Ile Gly His Ile Ala Leu Leu Ala Pro Asp Gln Phe Ala Ala	
770 775 780	
cct tgg aaa tct tgg gta gct act ttc att gtg aaa gat ctt ctc atg	2462
Pro Trp Lys Ser Trp Val Ala Thr Phe Ile Val Lys Asp Leu Leu Met	
785 790 795	
aat gat cgg ctt cca ggg aaa aag aca act aaa ctt tgg gtt cca gat	2510
Asn Asp Arg Leu Pro Gly Lys Lys Thr Thr Lys Leu Trp Val Pro Asp	
800 805 810 815	
gaa gaa gta tct cct gag aca atg gtc aaa att cag gct att aaa atg	2558
Glu Glu Val Ser Pro Glu Thr Met Val Lys Ile Gln Ala Ile Lys Met	
820 825 830	
atg gtt cga tgg cta ctt gga atg aaa aat aat cac agt aaa tca gga	2606
Met Val Arg Trp Leu Leu Gly Met Lys Asn Asn His Ser Lys Ser Gly	
835 840 845	
act tct acc tta aga ttg cta aca aca ata ttg cat agt gat gga gac	2654
Thr Ser Thr Leu Arg Leu Leu Thr Thr Ile Leu His Ser Asp Gly Asp	
850 855 860	

FIG. 1-5

ttg aca gaa cag ggg aaa att agt aaa cca gat atg tca cgt ctg aga	2702
Leu Thr Glu Gln Gly Lys Ile Ser Lys Pro Asp Met Ser Arg Leu Arg	
865 870 875	
ctt gct gct ggg agt gct att gtg aag ctg gca caa gaa ccc tgt tac	2750
Leu Ala Ala Gly Ser Ala Ile Val Lys Leu Ala Gln Glu Pro Cys Tyr	
880 885 890 895	
cat gaa atc atc aca tta gaa caa tat cag cta tgt gca tta gct atc	2798
His Glu Ile Ile Thr Leu Glu Gln Tyr Gln Leu Cys Ala Leu Ala Ile	
900 905 910	
aac gat gaa tgc tat caa gta aga caa gtg ttt gcc cag aaa ctt cac	2846
Asn Asp Glu Cys Tyr Gln Val Arg Gln Val Phe Ala Gln Lys Leu His	
915 920 925	
aaa ggc ctt tcc cgt tta cgg ctt cca ctt gag tat atg gca atc tgt	2894
Lys Gly Leu Ser Arg Leu Arg Leu Pro Leu Glu Tyr Met Ala Ile Cys	
930 935 940	
gcc ctt tgt gca aaa gat cct gta aag gag aga aga gct cat gct agg	2942
Ala Leu Cys Ala Lys Asp Pro Val Lys Glu Arg Arg Ala His Ala Arg	
945 950 955	
caa tgt ttg gtg aaa aat ata aat gta agg cgg gag tat ctg aag cag	2990
Gln Cys Leu Val Lys Asn Ile Asn Val Arg Arg Glu Tyr Leu Lys Gln	
960 965 970 975	
cat gca gct gtt agt gaa aaa tta ttg tct ctt cta cca gag tat gtt	3038
His Ala Ala Val Ser Glu Lys Leu Leu Ser Leu Leu Pro Glu Tyr Val	
980 985 990	
gtt cca tat aca att cac ctt ttg gca cat gac cca gat tat gtc aaa	3086
Val Pro Tyr Thr Ile His Leu Leu Ala His Asp Pro Asp Tyr Val Lys	
995 1000 1005	
gta cag gat att gaa caa ctt aaa gat gtt aaa gaa tgt ctt tgg ttt	3134
Val Gln Asp Ile Glu Gln Leu Lys Asp Val Lys Glu Cys Leu Trp Phe	
1010 1015 1020	
gtt ctg gaa ata tta atg gct aaa aat gaa aat aac agt cac gct ttt	3182
Val Leu Glu Ile Leu Met Ala Lys Asn Glu Asn Asn Ser His Ala Phe	
1025 1030 1035	

FIG. 1-6

atc aga aag atg gta gaa aat att aaa caa aca aaa gat gcc caa gga Ile Arg Lys Met Val Glu Asn Ile Lys Gln Thr Lys Asp Ala Gln Gly 1040 1045 1050 1055	3230
cca gat gat gca aaa atg aat gaa aaa ctg tac act gtg tgt gat gtt Pro Asp Asp Ala Lys Met Asn Glu Lys Leu Tyr Thr Val Cys Asp Val 1060 1065 1070	3278
gcc atg aat atc atc atg tca aag agt act aca tac agt ttg gaa tct Ala Met Asn Ile Ile Met Ser Lys Ser Thr Thr Tyr Ser Leu Glu Ser 1075 1080 1085	3326
cct aaa gac ccg gta cta cca gct cgt ttc ttc act caa cct gac aag Pro Lys Asp Pro Val Leu Pro Ala Arg Phe Phe Thr Gln Pro Asp Lys 1090 1095 1100	3374
aat ttc agt aac acc aaa aat tat ctg cct cct gaa atg aaa tca ttt Asn Phe Ser Asn Thr Lys Asn Tyr Leu Pro Pro Glu Met Lys Ser Phe 1105 1110 1115	3422
ttc act cct gga aaa cct aaa aca acc aat gtt cta gga gct gtt aac Phe Thr Pro Gly Lys Pro Lys Thr Thr Asn Val Leu Gly Ala Val Asn 1120 1125 1130 1135	3470
aag cca ctt tca tca gca ggc aag caa tct cag acc aaa tca tca cga Lys Pro Leu Ser Ser Ala Gly Lys Gln Ser Gln Thr Lys Ser Ser Arg 1140 1145 1150	3518
atg gaa act gta agc aat gca agc agc agc tca aat cca agc tct cct Met Glu Thr Val Ser Asn Ala Ser Ser Ser Ser Asn Pro Ser Ser Pro 1155 1160 1165	3566
gga aga ata aag ggg agg ctt gat agt tct gaa atg gat cac agt gaa Gly Arg Ile Lys Gly Arg Leu Asp Ser Ser Glu Met Asp His Ser Glu 1170 1175 1180	3614
aat gaa gat tac aca atg tct tca cct ttg ccg ggg aaa aaa agt gac Asn Glu Asp Tyr Thr Met Ser Ser Pro Leu Pro Gly Lys Lys Ser Asp 1185 1190 1195	3662
aag aga gac gac tct gat ctt gta agg tct gaa ttg gag aag cct aga Lys Arg Asp Asp Ser Asp Leu Val Arg Ser Glu Leu Glu Lys Pro Arg 1200 1205 1210 1215	3710

FIG. I-7

ggc agg aaa aaa acg ccc gtc aca gaa cag gag gag aaa tta ggt atg	3758
Gly Arg Lys Lys Thr Pro Val Thr Glu Gln Glu Glu Lys Leu Gly Met	
1220 1225 1230	
gat gac ttg act aag ttg gta cag gaa cag aaa cct aaa ggc agt cag	3806
Asp Asp Leu Thr Lys Leu Val Gln Glu Gln Lys Pro Lys Gly Ser Gln	
1235 1240 1245	
cga agt cgg aaa aga ggc cat acg gct tca gaa tct gat gaa cag cag	3854
Arg Ser Arg Lys Arg Gly His Thr Ala Ser Glu Ser Asp Glu Gln Gln	
1250 1255 1260	
tgg cct gag gaa aag agg ctc aaa gaa gat ata tta gaa aat gaa gat	3902
Trp Pro Glu Glu Lys Arg Leu Lys Glu Asp Ile Leu Glu Asn Glu Asp	
1265 1270 1275	
gaa cag aat agt ccg cca aaa aag ggt aaa aga ggc cga cca cca aaa	3950
Glu Gln Asn Ser Pro Pro Lys Lys Gly Lys Arg Gly Arg Pro Pro Lys	
1280 1285 1290 1295	
cct ctt ggt gga ggt aca cca aaa gaa gag cca aca atg aaa act tct	3998
Pro Leu Gly Gly Gly Thr Pro Lys Glu Glu Pro Thr Met Lys Thr Ser	
1300 1305 1310	
aaa aaa gga agc aaa aaa aaa tct gga cct cca gca cca gag gag gag	4046
Lys Lys Gly Ser Lys Lys Lys Ser Gly Pro Pro Ala Pro Glu Glu Glu	
1315 1320 1325	
gaa gaa gaa gaa aga caa agt gga aat acg gaa cag aag tcc aaa agc	4094
Glu Glu Glu Glu Arg Gln Ser Gly Asn Thr Glu Gln Lys Ser Lys Ser	
1330 1335 1340	
aaa cag cac cga gtg tca agg aga gca cag cag aga gca gaa tct cct	4142
Lys Gln His Arg Val Ser Arg Arg Ala Gln Gln Arg Ala Glu Ser Pro	
1345 1350 1355	
gaa tct agt gca att gaa tcc aca cag tcc aca cca cag aaa gga cga	4190
Glu Ser Ser Ala Ile Glu Ser Thr Gln Ser Thr Pro Gln Lys Gly Arg	
1360 1365 1370 1375	
gga aga cca tca aaa acg cca tca cca tca caa cca aaa aaa aat gtg	4238
Gly Arg Pro Ser Lys Thr Pro Ser Pro Ser Gln Pro Lys Lys Asn Val	
1380 1385 1390	

FIG. 1-8

taagttgtaa atattacatt tcaaaccaat ttcaaattat ttgcaaaag ttcctaaatt 4298
End

tgtaaacata catattgctg tatttaaatt ccatatattt agccccatta cactaggtac 4358

ggcggcgaag tgctaaaagg gaacggcgat gaacaaatgt aattaataac tttctctgtg 4418

aaagctttgg aaaaatcttt tttttttttt tttttttttg gtcaagcttg aggctgaata 4478

aagcctttga tgcacaaaat gggactgctg aagagtggac agttggacct tactttggtg 4538

accccatata tttgtggtca catgctttag ccatacacat ggtaacattg actatggagt 4598

cttgtgaaag tgtaatgtgc gatggctatg tagacataaa gaagaaactt gtaaatatct 4658

tttttctttt ttttaatggt tctgatttct gaagtgcctg tatagctttt atctgcggct 4718

ttaaactgac agtaccgcac tgtttattgg atctattgat ttgaaaagaa tttgttagga 4778

tagatcttaa gcagtaatct gtcagtgttt gtatttgtat tttctgcaat tttactgtga 4838

aaaaaaattt gttttcaaca attgggtgtca ttttcttgat gtcactattt gttggagagt 4898

taaatggtct cttccctttg tgtatcttac ctagtggtta ctctgggca cccttaatct 4958

tcagaggtgc taaattgtct gccattacac cagaaggatg cctctgatag gaggacaacc 5018

atgcaaattg tgaaatagtc ctgaagtctt tggattactt tacacctcag tattgatttg 5078

tcccagaatt ttctggcctt tcatggcaat gaaaatttta agaagaaaga tttaaagtat 5138

tttaatttta aagagtgtgt tataaaataa tgtactgaat tctttatccc attttatcat 5198

cctttcagtt tttattaatc tactgtatca ataaaattct gtaatttgaa tgagtaaaaa 5258

aaaaaaaaaa aaa 5271

FIG. 1-9



55		117
LYLNLAHLASDFELKHPGKDVRLVACCLADIIRIYAPEAPYTSBDKLDIEMFITRQLKGL		
196	217	241
LDTVLVNLVPAHKNLNKQAYDL		
		277
		LMLGKTSISDLSSEHVFDDLLELYNIDSHLLLSVLPOL
319	355	375
LGRFNDIHVPRLLECVPKASHCLMNHDPDLAKDLTEYL		
		404
		VTAAKKDILLVNDHLLNFVRERTLDDKRRV

FIG. 2

Hank's
conserved
regions:

Subdomain I

Subdomain II

Subdomain III

Consensus:	Mg-ATP binding loop		β-strand 2	β-strand 3	α-helix C
	(G x G x x G x V)			(x x x K x x x)	(x x x x E x x x)
AS3 position:	419	426	453	472	489
AS3 sequence:	YALQ.SA	GKDAKQI	LVVERIF	ERM K CLYLYA	VKALN E MWKC
Similar protein kinase sequences:	YTLGVSA (Elm I) YALINLL (Tsl) YHLKQNI (Cdc15) YKLVRKI (CK1a) IVLQESI (Alk5)	GedrfGKV (Ror2) GSGsfGdI (CK1a) AeGeshiS (Ypka) HesdfseV (MikI)	LLYEIMD (Yk1516) YLGEQVS (PKN2) YLCICLN (BCKI)	YAM K CLKKDV I (CeTPAI) YAM K CLDKKRI (bARKI) YAM K CLDKKRI (DmGPRKI) VAI K CIAKKAL (CamKI)	QAFKN K MQVL (AraI) TLALN E RIML (bARKI) YTRVR E IKFI (SMEI)

Hank's
conserved
regions:

Subdomain IV

Subdomain V

Subdomain VIa

Consensus:	β-strand 4	β-strand 5	α-helix D	α-helix E
AS3 position:	509	525	540	554
AS3 sequence:	LIDIVKDP	IESK.VMV	GKAQDEMKK	EDDEKIRKQ.LEVL
Similar protein kinase sequences:	LIDIVKDP (TPCKII) LIDWEFERP (PimI) LLGLCREA (Klg) LVKLIGYC (APKI)	IESCLVME (PvpKI) KESCLVME (Gila) KESCLVME (ZmPPK) KESCLVME (ZmPPK)	GNLQNEFLKL (Let23) GSLQNEFLRE (TORSO) GNLQEYLTR (TGfbRII)	ERDADAVKQILEA (CaMKIV) ECDANIMKQILSG (PICPK) ADQLNIAKQISAG (TORRTK) ESVIMYTKQLLL (NPKI)

FIG. 3

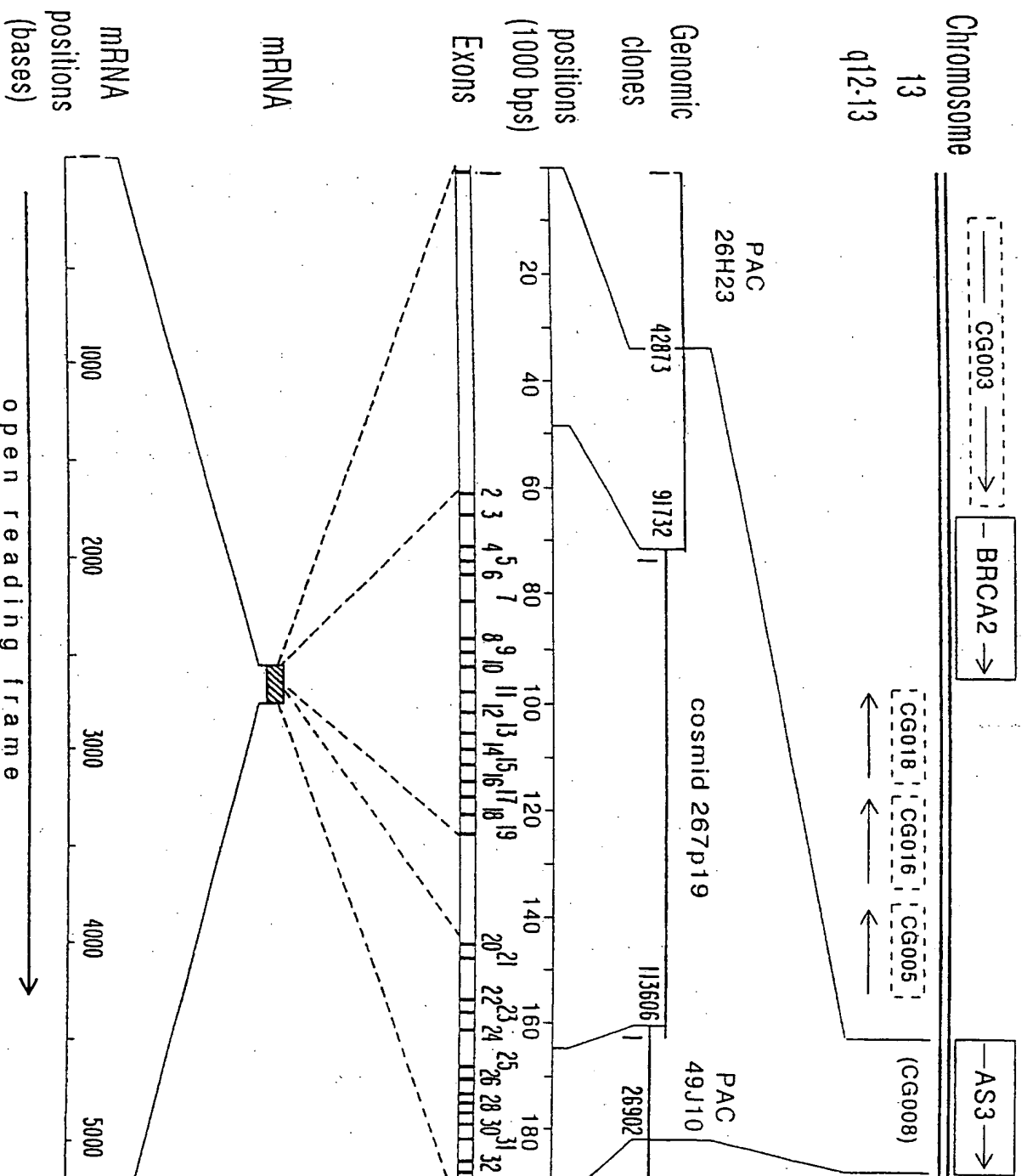


FIG. 4

{42873}	1	46	{42919}
CCGGAGAG.... Exon 1ACCCGGAG * gtaggaa...			
(13347)	47	173	(13475)
....ttttcttgtttcag * GGGTAGAA.... Exon 2GATTAAAG * gtgagta...			
(16397)	174	377	(16602)
..ttttatTTTTgtatag * ATGGTTGT.... Exon 3AACTAAAG * gcaagta...			
(22832)	378	464	(22920)
..tctTTTTTTattttaag * GATATATT.... Exon 4TACTTGAG * gtaagca...			
(23028)	465	562	(23125)
.....ccttatttttag * AACATTGC.... Exon 5GTTATAAA * gtaagtt...			
(23747)	563	689	(23873)
.....ttttgaattgcag * CAATGGCC.... Exon 6CTCATAAG * gtgagta...			
(32357)	690	854	(32439)
....tttatgtttttcag * AATTTAAA.... Exon 7TTACCACT * gtaagtc...			
(37809)	855	911	(37951)
...ctttctcctcaaaag * TTTTTTAA.... Exon 8AATTAAAG * gtaactt...			
(40437)	912	1027	(40554)
.....ttttattttag * AGCAATGA.... Exon 9TTGGGCAG * gtatatg...			
(43428)	1028	1122	(43524)
...tttatattttatcag * GTTTAATG.... Exon 10....CTTAACAG * gtactat...			
(48471)	1123	1268	(48617)
.....tgttatctttcag * AGTATCTT.... Exon 11....ACAAACGA * gtaagta...			
(51727)	1269	1420	(51880)
....tttttgtttttaag * TGGAGAGT.... Exon 12....GATGATCG * gtaagtt...			
(53049)	1421	1534	(53164)
...tctgctttttttag * ACTACTTG.... Exon 13....GCTGTGAA * gtatggt...			

FIG. 5-1

(58816) 1535	1616 (58898)
....tttgtgtttttcag * AGCATTGA.... Exon 14....	AACCCAAA * gtaagta...
(61447) 1617	1665 (61497)
...ttgtgtgattttacag * ACAGATGC.... Exon 15....	TATTACAA * gtaagtt...
(64323) 1666	1805 (64464)
.....tttattttaag * GAAATTTA.... Exon 16....	GTTGTGTG * gtaagga...
(65916) 1806	1921 (66033)
...taatctgtattacag * CGTGAAAT.... Exon 17....	TCTATCAG * gtatttg...
(71527) 1922	2027 (71633)
...ttggtcatatttttag * TGCTCTTA.... Exon 18....	TGCTTAAG * gtaagta...
(74539) 2028	2188 (74700)
...tgattcatttttatag * GTACTCTC.... Exon 19....	ATCAGATC * gtgagtt...
(96694) 2189	2312 (96818)
....tttttttttaatatag * AGCCTTGC.... Exon 20....	TATTTGAG * gtaatga...
(99765) 2313	2471 (99925)
...tcccctcattttcag * CCTCTGCA.... Exon 21....	ATGATCGG * gtaattt...
(105674) 2472	2540 (105744)
...ctcgtttatatttttag * CTTCCAGG.... Exon 22....	TGGTCAAA * gtgagta...
(107185) 2541	2677 (107322)
...ttgtctcttaaatatag * ATTCAGGC.... Exon 23....	AAAATTAG * gtatgca...
(110571) 2678	2801 (110696)
...ctactcattttttcag * TAAACCAG.... Exon 24....	CTATCAAC * gtaagga...
[4319] 2802	3006 [4524]
....ttgtgtctttacag * GATGAATG.... Exon 25....	TGTTAGTG * gtaagca...

FIG. 5-2

[6829]	3007	3121	[6945]
.....ttttcttttttcag *	AAAAATTA.... Exon 26....	GTAAAGA *	gtaagac...
[9074]	3122	3254	[9208]
.....tttttttttttttag *	ATGTCTTT.... Exon 27....	TGAATGAA *	gtatgta...
[9522]	3255	3374	[9642]
.....tatactattgcag *	AAACTGTA.... Exon 28....	CTGACAAG *	gtagtta...
[10614]	3375	3437	[10679]
...ttctcttggtttag *	AATTCAG.... Exon 29....	CTGGAAAA *	gtatggt...
[11561]	3438	3583	[11709]
...catttctcatttcag *	CCTAAAAC.... Exon 30....	AAGGGGAG *	gtaagtg...
[15476]	3584	3689	[15583]
...tgtctgtattaaaag *	GCTTGATA.... Exon 31....	TTGTAAGG *	gtgagat...
[21107]	3690	4129	[21548]
...ttttttttcccctag *	TCTGAATT.... Exon 32....	CAGCAGAG *	gtaagca...
[21640]	4130	4354	[21866]
...tcttccccaagcag *	AGCAGAAT.... Exon 33....	TACACTAG *	gtaagat...
[26002]	4355	5253	[26902]
.....ctttcctttttaag *	GTACGGCG.... Exon 34....	GAATGAGT *	(poly-A)

FIG. 5-3